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Image Problem Mailbox.**

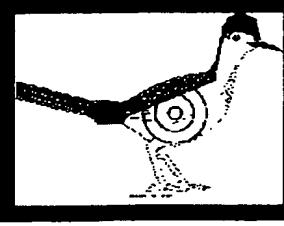


FIG. 1

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File Edit View Go Communicator Help

Bookmarks Location http://victoria.inpharmatica.co.uk/~volker/BPD3target.html

 Target Mining Interface



Select Your Query Sequence

• Enter PDB accession number (e.g. 1QMA): 1fa and chain (e.g. B): a

OR

• Enter one Swiss-Prot accession (e.g. P27504) or GenBank proteinID (e.g. CAB08761.1):

Select Database

Release: DEVF9 = BPD3

Apply Filters

• Iteration Filter: PSI-BLAST matches to be excluded:
 Matches detected during the first 20 forward iterations

If you select e.g. "Matches detected during the first 3 iterations" these matches will be excluded from the report (using the first_PB_iter annotation). This allows you to focus on more remote homologous which have been detected after 4 or more PSI-BLAST iterations. Matches detected using PSI-BLAST with negative iterations or using Genome-Threader are not effected by this option. However, if one match is found during the first e.g. 3 PSI-BLAST iterations and by Genome-Threader it will be excluded.

• Filter for the following SPECIES:

Homo sapiens Rattus norvegicus (Rat) Mus musculus (Mouse) Danio rerio (Zebra fish)

100% 

FIG. 2A

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Accession	Residuum Sequence display	BPD link	W3W link	Title	Organism	Div	% ID	Query resn.	Target resn.	AJn. score	Conf.
J	Red Seq. View AAF71133.1 drill through Top50BlastHits	AAF71133.1		PRO2769	Homo sapiens	PRI	13.8% unmaskedSW	109-179	1-80	122	100% unmaskedGT
J	Red Seq. View CA852192.1 drill through Top50BlastHits	CA852192.1		G7c protein	Homo sapiens	PRI	9.6% unmaskedSW	7-117	20-124	82	99.18% unmaskedGT
J	Red Seq. View CAA829101.1 drill through Top50BlastHits	CAA829101.1		basic transcription factor 2, 44 kD subunit	Homo sapiens	PRI	11.2% unmaskedSW	5-164	61-225	75	99.08% unmaskedGT
J	Red Seq. View AAD21820.1 drill through Top50BlastHits	AAD21820.1		NC37	Homo sapiens	PRI	9.6% unmaskedSW	7-117	318-422	82	98.86% unmaskedGT
J	Red Seq. View BA22076.1 drill through Top50BlastHits	BA22076.1		Not given	Homo sapiens	PRI	16.4% unmaskedSW	5-114	1836-1950	78	99.52% unmaskedGT
J	Red Seq. View AAA36154.1 drill through Top50BlastHits	AAA36154.1		Not given	Homo sapiens	PRI	13.2% unmaskedSW	5-112	10-137	73	98.16% unmaskedGT
J	Red Seq. View AAFD3046.1 drill through Top50BlastHits	AAFD3046.1		candidate tumor suppressor protein DICE1	Homo sapiens	PRI	13.8% unmaskedSW	5-113	4-131	79	97.07% unmaskedGT
→	Red Seq. View AAC74854.1 drill through Top50BlastHits	AAC74854.1		orf, hypothetical protein	Escherichia coli	BCT	16.7% unmaskedSW	5-99	250-335	78	95.09% unmaskedGT
J	Red Seq. View AA860942.1 drill through Top50BlastHits	AA860942.1		breast cancer suppressor candidate 1	Homo sapiens	PRI	16.2% unmaskedSW	63-156	2-90	80	93.33% unmaskedGT
J	Red Seq. View AA467537.1 drill through Top50BlastHits	AA467537.1		glycoprotein IIIa	Homo sapiens	PRI	18.9% unmaskedSW	3-112	111-251	72	92.08% unmaskedGT reverse Hit
J	Red Seq. View AA52589.1 drill through Top50BlastHits	AA52589.1		Not given	Homo sapiens	PRI	19.6% unmaskedSW	3-112	138-277	74	91.34% unmaskedGT reverse Hit
J	Red Seq. View AA871380.1 drill through Top50BlastHits	AA871380.1		platelet membrane glycoprotein IIIa beta subunit	Homo sapiens	PRI	19.6% unmaskedSW	3-112	138-277	74	91.34% unmaskedGT reverse Hit
J	Red Seq. View AA435927.1 drill through Top50BlastHits	AA435927.1		Not given	Homo sapiens	PRI	19.6% unmaskedSW	3-112	138-277	74	91.34% unmaskedGT

FIG. 2B
1) 509 hits identified by Genome Threader only:

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FIG. 4

File Edit View Go Communicator Help

Book Forward Reload Home Search Netscape Print Security Stop

Bookmarks Location: http://www.sanger.ac.uk/cgi-bin/Pfam/nph-search.cgi

The Sanger Centre **Pfam**
Protein families database of alignments and HMMs

Home | Keyword search | Protein search | DNA search | Browse Pfam | Taxonomy search | Help

Results for gi|1788084|gb|AAC74854.1|

There were no matches to Pfam-A (including borderline matches) for gi|1788084|gb|AAC74854.1|

Matches to Pfam-B

Domain	Start	End	Evalue	Alignment
Pfam-B_39416	233	423	3.7e-103	Align

[427 residues]

Alignments of Pfam-B domains to best-matching Pfam-B sequence

Format for fetching alignments to Pfam-B families Hypertext linked to swisspfam

Query gi|1788084|gb|AAC74854.1|/233-423 matching Pfam-B_39416

YEAM_ECOLI 233 DLRYKNYEKRDPDSSQAVMFCLMDVSGSMDQSTKDMAKRFYILLYLFLSR 282
gi|1788084|gb|AAC74854.1| 233 DLRYKNYEKRDPDSSQAVMFCLMDVSGSMDQSTKDMAKRFYILLYLFLSR 282

YEAM_ECOLI 283 TYKNVEVVYIRDMTQAKEVDEHEFFYSQETGGTIVSSALKLMDDEVVKERY 332
gi|1788084|gb|AAC74854.1| 283 TYKNVEVVYIRDMTQAKEVDEHEFFYSQETGGTIVSSALKLMDDEVVKERY 332

YEAM_ECOLI 333 NPAQWNIYRAQASDGDNWADDSPLCHEILAKLLPVVRYYSYIEITRRAM 382
gi|1788084|gb|AAC74854.1| 333 NPAQWNIYRAQASDGDNWADDSPLCHEILAKLLPVVRYYSYIEITRRAM 382

YEAM_ECOLI 383 QTLWREYEMLQSTFDHFMQHIRDQDDIYPVFRELFHKQNA 423
gi|1788084|gb|AAC74854.1| 383 QTLWREYEMLQSTFDHFMQHIRDQDDIYPVFRELFHKQNA 423

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100%

FIG. 5

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Bookmarks Location <http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?cmd=Retrieve&db=...>

LOCUS ARCA74854 427 aa BCT 01-DEC-2000
 DEFINITION orf, hypothetical protein [Escherichia coli K12].
 ACCESSION ARCA74854
 PID g1788084
 VERSION ARCA74854.1 GI:1788084
 DBSOURCE locus AE000273 accession AE000273.1
 KEYWORDS
 SOURCE Escherichia coli K12.
 ORGANISM Escherichia coli K12
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia.
 REFERENCE 1 (residues 1 to 427)
 AUTHORS Blattner, F.R., Plunkett, G., III, Bloch, C.A., Perna, N.T., Burland, V.,
 Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F.,
 Gregor, J., Davis, N.W., Kirkpatrick, M.A., Goeden, M.R., Rose, D.J.,
 Mau, B. and Shao, Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 97426617
 MEDLINE 9278503
 PUBMED
 REFERENCE 2 (residues 1 to 427)
 AUTHORS Blattner, F.R.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
 University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
 Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
 608-263-7459
 REFERENCE 3 (residues 1 to 427)
 AUTHORS Blattner, F.R.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
 University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
 Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax:
 608-263-7459
 REFERENCE 4 (residues 1 to 427)
 AUTHORS Plunkett, G. III.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-1998) Laboratory of Genetics, University of
 Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
 COMMENT This sequence was determined by the E. coli Genome Project at the
 University of Wisconsin-Madison (Frederick R. Blattner, director).
 Supported by NIH grants HG00301 and HG01428 (from the Human Genome
 Project and NCMGR). The entire sequence was independently
 determined from E. coli K12 strain MG1655. Predicted open reading
 frames were determined using GeneMark software, kindly supplied by
 Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA,
 30332 [e-mail: [mark@amber.gatech.edu">mark@amber.gatech.edu](mailto:mark@amber.gatech.edu)]. Open reading frames that
 have been correlated with genetic loci are being annotated with CG
 Site Nos., unique ID nos. for the genes in the E. coli Genetic
 Stock Center (CGSC) database at Yale University, kindly supplied by
 Mary Berlyn. A public version of the database is accessible
 (<http://cgsc.biology.yale.edu>). Annotation of the genome is an
 ongoing task whose goal is to make the genome sequence more useful
 by correlating it with other data. Comments to the authors are
 appreciated. Updated information will be available at the E. coli
 Genome Project's World Wide Web site
 (<http://www.genetics.wisc.edu>). *** The E. coli K12 sequence and
 its annotations are periodically updated; this is version M54. No
 sequence changes. Annotation updates: updated gene identifications
 and products; all new functional assignments courtesy of Monica
 Riley; added promoters, protein binding sites, and repeated
 sequences described in reference 1. The unique numeric identifiers
 beginning with a lowercase 'b' assigned to each gene (protein- or
 RNA-encoding) are now designated as gene synonyms instead of
 labels. This should allow them to be searched for in Entrez as gene
 names.
 FEATURES Method: conceptual translation.
 source Location/Qualifiers
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 /organism="Escherichia coli K12"
 /strain="K12"
 /sub_strain="MG1655"
 /db_xref="taxon:83333"
 Protein 1..427
 /function="orf; Unknown"
 /product="orf, hypothetical protein"
 CDS 1..427
 /gene="yeaM"
 /coded_by="1788078:6385..7668"
 /transl_table=11
 /note="0427: This 427 aa ORF is 28 pct identical (43 gaps)
 to 327 residues of an approx. 312 aa protein YZDC_BACSU
 SW: P45742"
 ORIGIN 1 mtwfidrrln gknksmvnrq rflrrykaqi kqsisceaink rsvidvdsge svsiptedis
 61 epmfhggrrgg lhrvhpgnd hfvqndrier pgggggsgs gqqgasqdge gqdefvfqis
 121 kdeyldilfe dhalpnlkqn qqrqlteykt hragytangv panisvvrsl qnsllarrtam
 181 tackrrelha leenlaiisn sepaqlleee rlrkeiaelr akiervpfid tfdlryknye

FIG. 6A

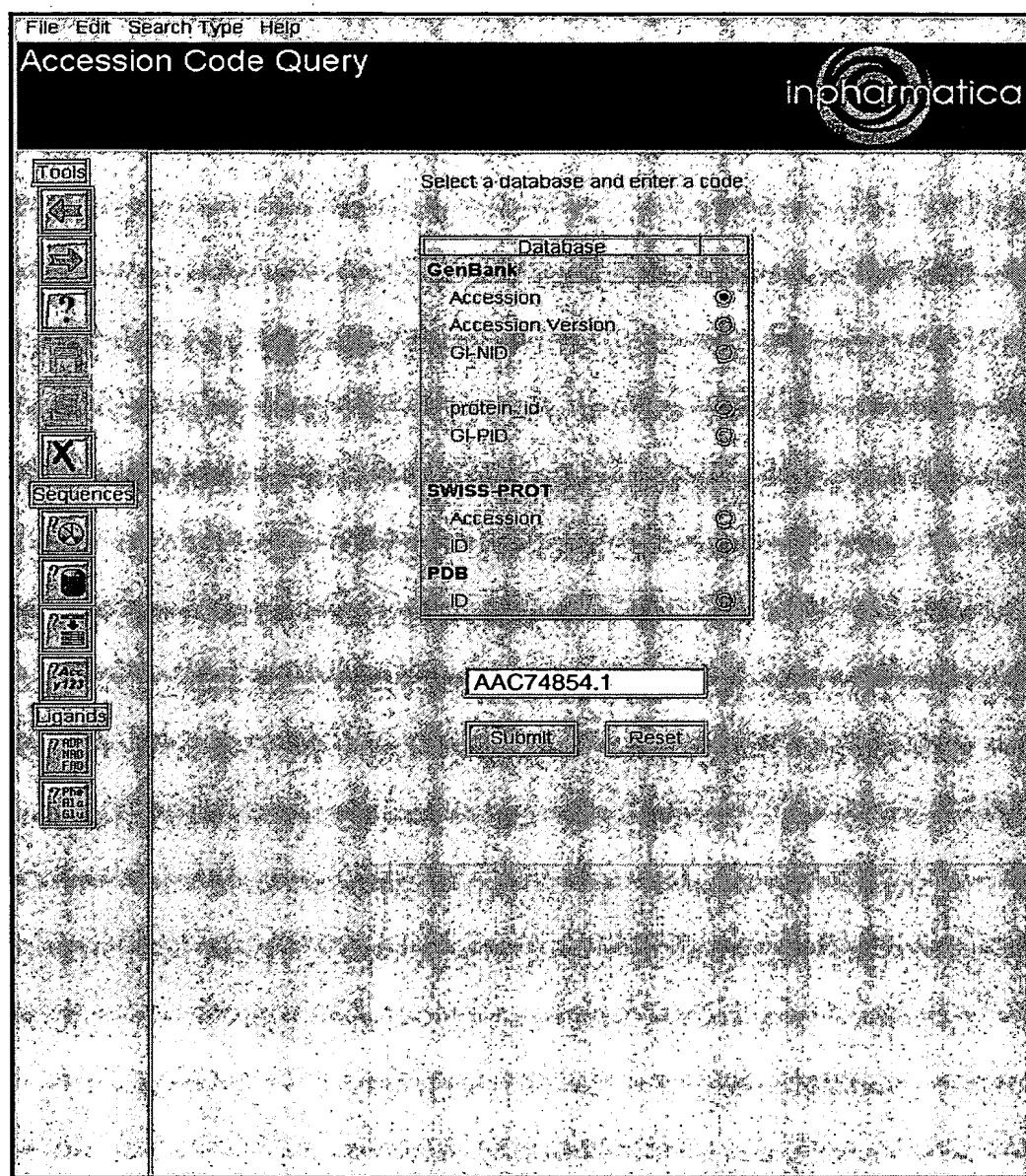


FIG. 6C Aligned Sequence Display

Query details:
AAC74854.1: orf, hypothetical protein

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inpharmatica

Reverse Maximised PSI-BLAST results:

Total selected: 0

View alignment

Page 1 of 1 Total hits: 2 Selected: 0

Cluster Detail

Cluster	Detail	Code	Line	Line	Organism	%ID	Query	Target	Length	E-value
•		CAB12726.1	Not given		<i>B. suis</i>	23.0	14 - 423	2 - 385	1	2.00E-29
•		AAK59860.0	Conserved hypothetical protein	23.0	<i>M. marmoreum</i>	15.0	734 - 771	259 - 401	-8	4.00E-03

Tools

Sequences

Ligands

GenBank SWISSPROT PDB

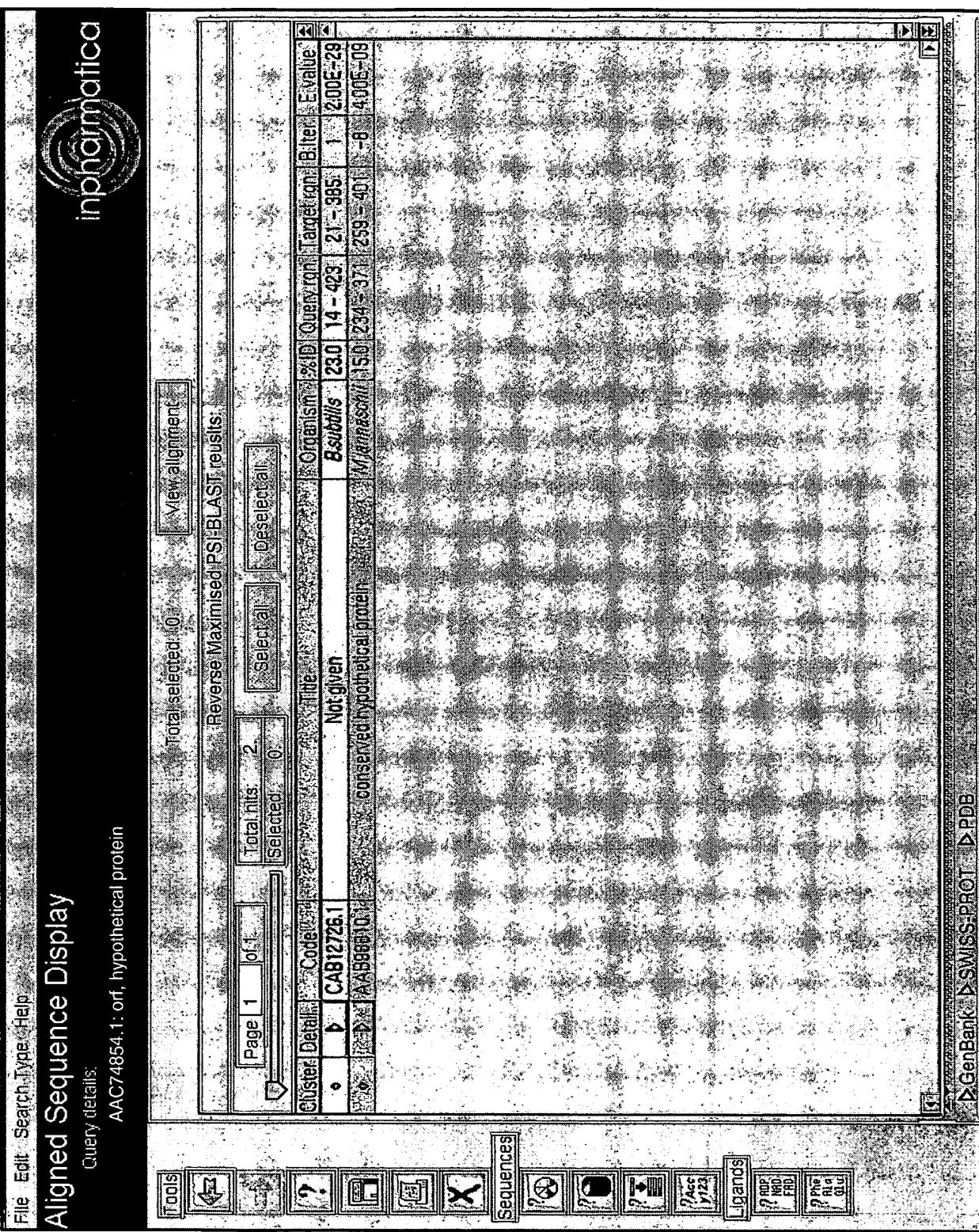
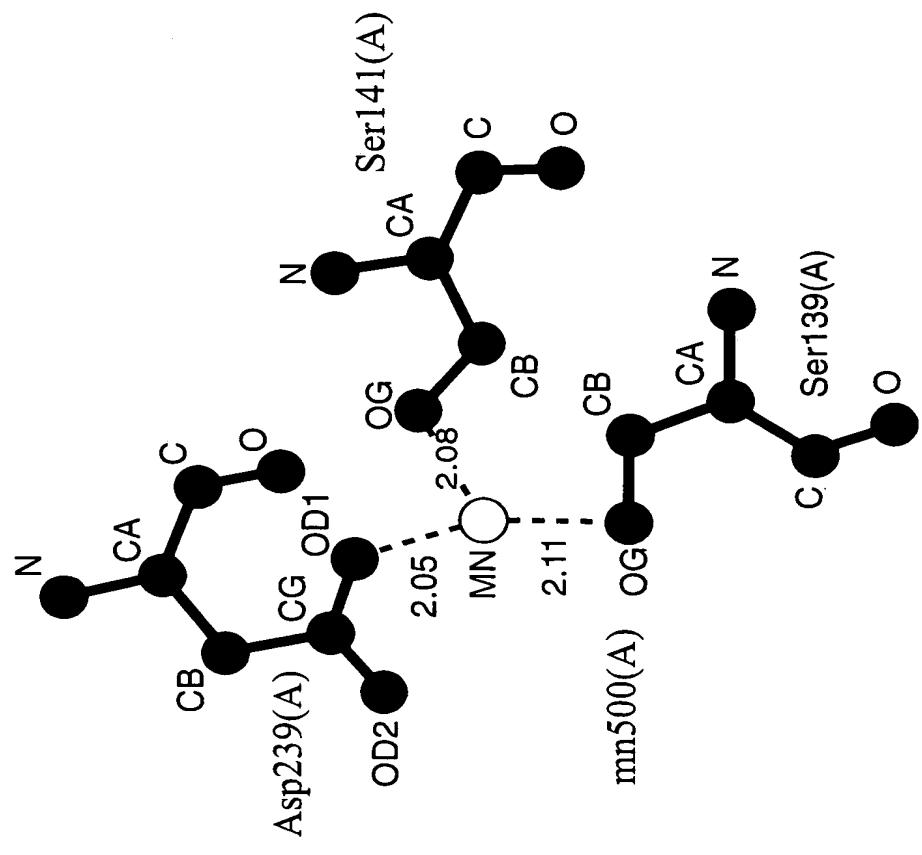


FIG. 7
AlEye output (January 4, 2002 3:07 PM)

FIG. 8A



11fa: Mn500 Chain [Å]

FIG. 8B

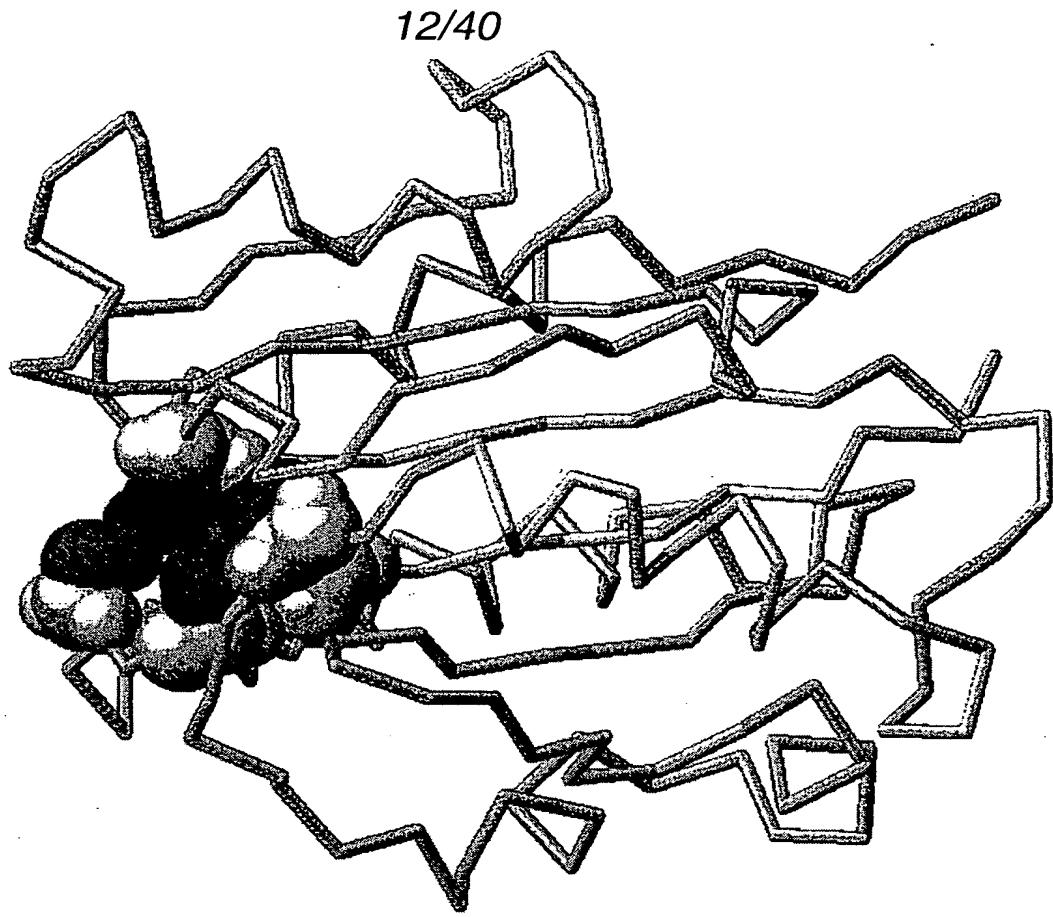
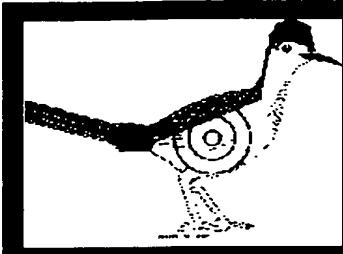


FIG. 9

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Bookmarks Location: http://victoria.inpharmatica.co.uk/~volker/BPD3target.html

 Target Mining Interface

 inpharmatica

Select Your Query Sequence

- Enter PDB accession number (e.g. 1QMA): and chain (e.g. B):

OR

- Enter one Swiss-Prot accession (e.g. P27504) or GenBank proteinID (e.g. CAB08761.1):

Select Database

Release:

Apply Filters

- Iteration Filter: PSI-BLAST matches to be excluded:

If you select e.g. "Matches detected during the first 3 iterations" these matches will be excluded from the report (using the first_PB_iter annotation). This allows you to focus on more remote homologous which have been detected after 4 or more PSI-BLAST iterations. Matches detected using PSI-BLAST with negative iterations or using Genome-Threader are not effected by this option. However, if one match is found during the first e.g. 3 PSI-BLAST iterations and by Genome-Threader it will be excluded.

FIG. 10A

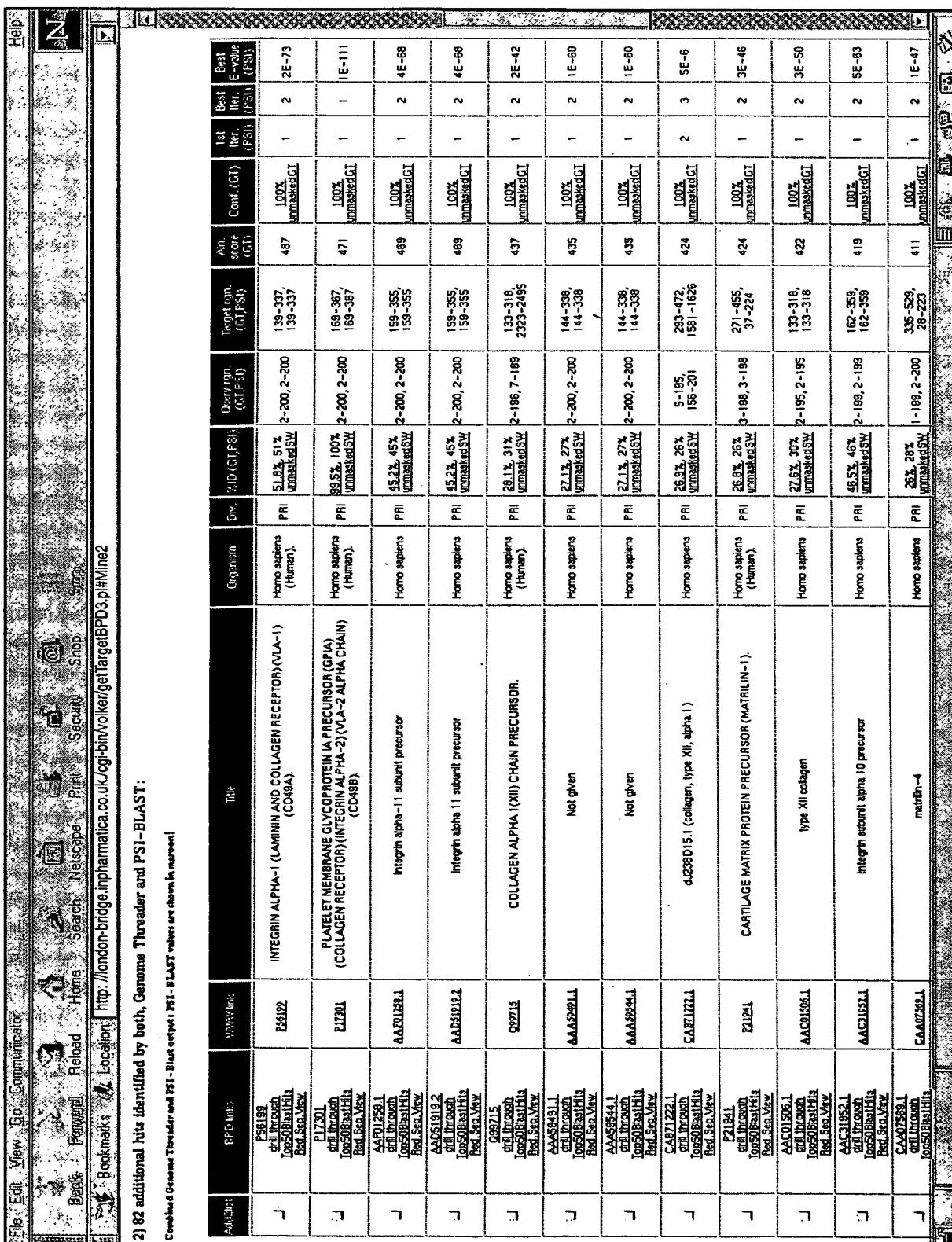


FIG. 10B

		GT		Confidence			
		PRI	unmasked SW	PRI	unmasked SW	PRI	unmasked GT
1	<u>Top50BlastHits</u>	<u>BAA91707_1</u>	Not given			142	<u>100%</u> <u>unmasked GT</u>
	Red Seq View						
1	<u>AAA36735_1</u> drill through <u>Top50BlastHits</u>	<u>AAA36795_1</u>	undulin 2	Homo sapiens	PRI 34.7%, 21% unmasked SW	2-46, 139-196	3-51, 37-93
	Red Seq View						
1	<u>AAD40367_1</u> drill through <u>Top50BlastHits</u>	<u>AAD40367_1</u>	calcium-activated chloride channel-2	Homo sapiens	PRI 15%, 15% unmasked SW	8-117,	312-421,
	Red Seq View						
1	<u>CAA67559_1</u> drill through <u>Top50BlastHits</u>	<u>CAA67559_1</u>	collagen VI-alpha-1 chain	Homo sapiens	PRI 21.1%, 21% unmasked SW	108-197, 108-197	7-92, 7-92
	Red Seq View						
1	<u>AAC76768_1</u> drill through <u>Top50BlastHits</u>	<u>AAC76768_1</u>	orf, hypothetical protein	Escherichia coli	BCT 13.2%, 11% unmasked SW	9-134, 7-186	267-384, 265-424
→	Red Seq View						
1	<u>CAB43000_1</u> drill through <u>Top50BlastHits</u>	<u>CAB43000_1</u>	tellurite resistance	Escherichia coli	BCT 12.9%, 14% unmasked SW	8-192, 2-181	214-398, 208-380
	Red Seq View						
1	<u>AAA6014_1</u> drill through <u>Top50BlastHits</u>	<u>AAA60114_1</u>	platelet membrane glycoprotein IIb	Homo sapiens	PRI 14%, 13% unmasked SW	157-199, 157-199	145-187, 145-187
	Red Seq View						

608 out of these 632 PSI-BLAST matches were identified using 'positive iterations'.

608 out of these 632 PSI-BLAST matches were identified using 'positive iterations'.

FIG. 10C

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24 out of these 632 PSI-BLAST matches were identified using 'negative iterations':

Inpharmatica

Redundant Sequence Display

Contains:
 2 Sub-sequences.
 0 PROSITE hits.
 0 PRINTS hits.

File Edit Search Type Help

Representative code: PQ3818 Length: 127 Organism name: Escherichia coli [...additional annotation]

Aligned sequences:

PQ3818	AAC76768.1
	AAA62097.1

Primary database information:

SWISS-PROT	Code	Details	Organism name : Escherichia coli
	PQ3818	Tax ID: 562	Gene Name: YEM
			EC Number: Not available
			Description: HYPOTHETICAL 43.6 kDa protein in sigma-K12 intergenic region
			Other links: ECOGENE, EGT, PIR, PIR-ALL

GenBank	Code	Details	Organism name : Escherichia coli
	AAC76768	Tax ID: 562	Gene Name: YEM
			EC Number: Not available
			Description: HYPOTHETICAL 43.6 kDa protein in sigma-K12 intergenic region

Sequences

Tools

Search

?

X

Sequences

Alignments

Print

Help

Start

FIG.

FIG. 12

Pfam
Protein families database of alignments and HMMs

[Home](#) | [Keyword search](#) | [Protein search](#) | [DNA search](#) | [Browse Pfam](#) | [Taxonomy search](#) | [Help](#)



Results for gi|2367274|gb|AAC76768.1|

There were no matches to Pfam-A (including borderline matches) for gi|2367274|gb|AAC76768.1|

Matches to Pfam-B

Domain	Start	End	Evalue	Alignment
Pfam-B_15204	204	408	2.4e-108	Align

[427 residues]

.....

Alignments of Pfam-B domains to best-matching Pfam-B sequence

Format for fetching alignments to Pfam-B families: Hypertext linked to swisspfam

Query gi|2367274|gb|AAC76768.1|204-408 matching Pfam-B_15204

```

YIEI_ECOLI 204 DILRLLPPELATLGITELEYEFYRRLVEKQLLTYRLNGESWREKVIERPV 253
DILRLLPPELATLGITELEYEFYRRLVEKQLLTYRLNGESWREKVIERPV
gi|2367274|gb|AAC76768.1| 204 DILRLLPPELATLGITELEYEFYRRLVEKQLLTYRLNGESWREKVIERPV 253

YIEI_ECOLI 254 VHKDYDEQPRGPPFIVCVDTSS6S667PHE0CAKAPCLALMRIMLAENRRCY 303
VHKDYDEQPRGPPFIVCVDTSS6S667PHE0CAKAPCLALMRIMLAENRRCY
gi|2367274|gb|AAC76768.1| 254 VHKDYDEQPRGPPFIVCVDTSS6S667PHE0CAKAPCLALMRIMLAENRRCY 303

YIEI_ECOLI 304 IMLFSTEIVRYELSGPQ61EQAIRFLSQQRG67DLASCYRAIMERLQSR 353
IMLFSTEIVRYELSGPQ61EQAIRFLSQQRG67DLASCYRAIMERLQSR
gi|2367274|gb|AAC76768.1| 304 IMLFSTEIVRYELSGPQ61EQAIRFLSQQRG67DLASCYRAIMERLQSR 353

YIEI_ECOLI 354 EWPDRDRWVISDFIRQLPDDVTSKVKEIQRVHQMRPMUVAMSAMGKPGI 403
EWPDRDRWVISDFIRQLPDDVTSKVKEIQRVHQMRPMUVAMSAMGKPGI
gi|2367274|gb|AAC76768.1| 354 EWPDRDRWVISDFIRQLPDDVTSKVKEIQRVHQMRPMUVAMSAMGKPGI 403

YIEI_ECOLI 404 MRLYD 408
MRLYD
gi|2367274|gb|AAC76768.1| 404 MRLYD 408

```

.....

If you think there is anything wrong with this script, please contact [Pfam](#)

FIG. 13

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File Edit View Go Communicator Help

Bookmarks Location: <http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?cmd=Retrieve&db=protein>

LOCUS RAC76768 427 aa BCT 01-DEC-2000
 DEFINITION orf, hypothetical protein [Escherichia coli K12].
 ACCESSION RAC76768
 PID g2367274
 VERSION RAC76768.1 GI:2367274
 DBSOURCE locus AE000451 accession AE000451.1
 KEYWORDS
 SOURCE Escherichia coli K12.
 ORGANISM Escherichia coli K12. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
 REFERENCE 1 (residues 1 to 427)
 AUTHORS Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V., Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F., Gregor, J., Davis, R.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J., Mau, B. and Shao, Y.
 TITLE The complete genome sequence of Escherichia coli K-12
 JOURNAL Science 277 (5331), 1453-1474 (1997)
 MEDLINE 97426617
 PUBMED 9278503
 REFERENCE 2 (residues 1 to 427)
 AUTHORS Blattner, F.R.
 TITLE Direct Submission
 JOURNAL Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
 REFERENCE 3 (residues 1 to 427)
 AUTHORS Blattner, F.R.
 TITLE Direct Submission
 JOURNAL Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA. Email: ecoli@genetics.wisc.edu Phone: 608-262-2534 Fax: 608-263-7459
 REFERENCE 4 (residues 1 to 427)
 AUTHORS Plunkett, G. III.
 TITLE Direct Submission
 JOURNAL Submitted (13-OCT-1998) Laboratory of Genetics, University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA
 COMMENT This sequence was determined by the *E. coli* Genome Project at the University of Wisconsin-Madison (Frederick R. Blattner, director). Supported by NIMH grants M600301 and M601428 (from the Human Genome Project and NCHGR). The entire sequence was independently determined from *E. coli* K12 strain M61655. Predicted open reading frames were determined using GeneMark software, kindly supplied by Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA, 30332 [e-mail: mark@amber.gatech.edu]. Open reading frames that have been correlated with genetic loci are being annotated with CG site nos., unique ID nos. for the genes in the *E. coli* Genetic Stock Center (CGSC) database at Yale University, kindly supplied by Mary Berklyn. A public version of the database is accessible (<http://cgsc.biology.yale.edu>). Annotation of the genome is an ongoing task whose goal is to make the genome sequence more useful by correlating it with other data. Comments to the authors are appreciated. Updated information will be available at the *E. coli* Genome Project's World Wide Web site (<http://www.genetics.wisc.edu>). *** The *E. coli* K12 sequence and its annotations are periodically updated; this is version M54. No sequence changes. Annotation updates: updated gene identifications and products; all new functional assignments courtesy of Monica Riley; added promoters, protein binding sites, and repeated sequences described in reference 1. The unique numeric identifiers beginning with a lowercase 'b' assigned to each gene (protein- or RNA-encoding) are now designated as gene synonyms instead of labels. This should allow them to be searched for in Entrez as gene names.
 Method: conceptual translation.
 FEATURES
 Source Location/Qualifiers
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 /strain="K12"
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 /db_xref="taxon:83333"
 Protein 1..427
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 CDS 1..427
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 /coded_by="complement(2367272..5249..6532)"
 /transl_table=11
 /note="f427; sequence change joins ORFs pied and piem from earlier version"
 ORIGIN 1 mrsrlkdav ppelteewmc yqqsqlistp qfivqlpqil dlhhrinspw aeqarqlvda
 61 nsttsalht lfliqrwlsl iqvattinqq lleeereqll sevgemats gglepiladn
 121 ntaagrlwdm sagqlkrgdy qliivkygef1 negpelkrla eqqlgrsreak siphndaqne
 181 tfrrtmvrep a tpeqvvdglq qsdilrlp relatioite lenefnrrlv sklltnr1b

FIG. 14A

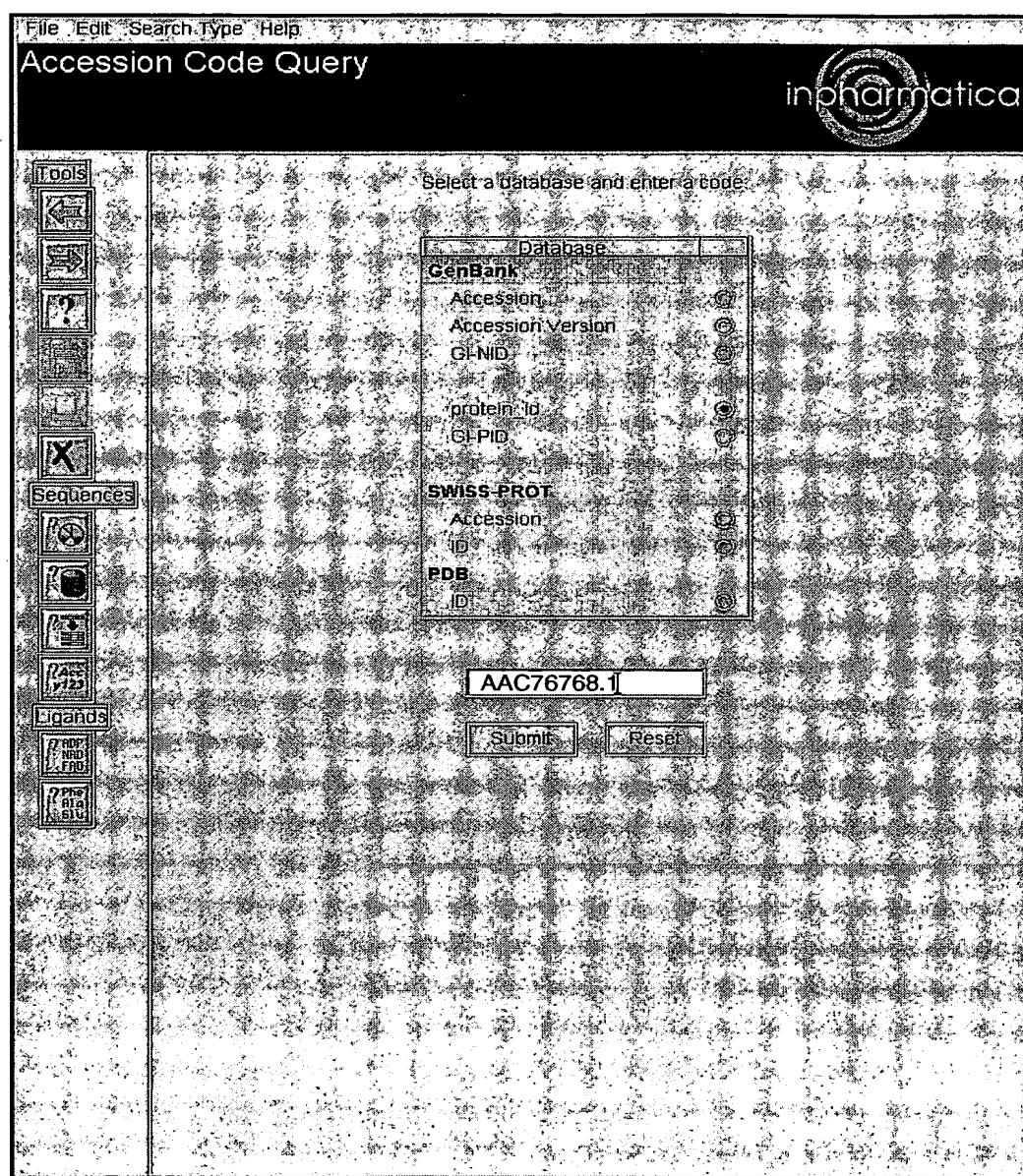


FIG. 14B Aligned Sequence Display

File Edit Search Type Help

Query details: AAC76768 1: oft hypothetical protein

FIG. 14C Aligned Sequence Display

[Query details](#) | [AAC76768.1: orf, hypothetical protein](#)

Aligned Sequence Display

AAC76768.1: orf, hypothetical protein

Query details: Total selected: 0

View alignment

Page 1 of 17 Total hits: 508 Selected: 0

Selected Deselect All

Reverse Maximised PSI-BLAST results

Cluster	Detail	Code	Title	Organism	PSI	Query	BitScore	Target	BitScore	Expect
•	►	BAA80016.1	452aa long hypothetical protein	<i>Arenicola</i>	280	156 - 407	202 - 431	2	2.00E-60	•
•	►	Q56486	HYPOTHETICAL PROTEIN M4017	<i>Thiobacillus</i>	22	146 - 405	122 - 381	3	2.00E-71	•
•	►	AAE88810.1	conserved hypothetical protein	<i>Manihot esculenta</i>	230	147 - 410	170 - 420	3	2.00E-65	•
•	►	AAE27880.1	putative tetrameric polypeptide	<i>Thiobacillus</i>	180	168 - 404	144 - 398	3	2.00E-51	•
•	►	Q55974	HYPOTHETICAL 45.6 kDa PROTEIN SLOUD03	<i>Ssp.</i>	240	241 - 407	175 - 186	3	4.00E-39	•
•	►	AAE88457.1	hypothetical protein	<i>Manihot esculenta</i>	240	51 - 370	324 - 535	3	5.00E-22	•
•	►	CAX30478.1	Not given	<i>Miniculus</i>	230	247 - 416	132 - 308	4	2.00E-44	•
•	►	AAE45502.1	Not given	<i>Escherichia coli</i>	160	128 - 412	107 - 305	4	3.00E-72	•
•	►	AAB24821.1	leucine rich alpha chain	<i>Aspergillus</i>	150	223 - 412	107 - 305	4	3.00E-42	•
•	►	11001	1 DOMAIN FROM INTEGRIN CTS1 YN2 BOUND	<i>Aspergillus</i>	160	283 - 412	111 - 158	4	2.00E-41	•
•	►	11001	1 DOMAIN FROM INTEGRIN CTS1 YN2 BOUND	<i>Aspergillus</i>	160	284 - 412	1 - 158	4	2.00E-41	•
•	►	11001	MAC-1 DOMAIN MAGNESIUM COMPLEX	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	110N2	MAC-1 DOMAIN METAL FREE	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	110N1	MAC-1 DOMAIN METAL FREE	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	18102	MAC-1 DOMAIN MAGNESIUM COMPLEX	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	18102	MAC-1 DOMAIN MAGNESIUM COMPLEX	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	181C1	MAC-1 DOMAIN CADMIUM COMPLEX	<i>Aspergillus</i>	160	284 - 412	2 - 158	4	3.00E-41	•
•	►	Q22433	MAGNESIUM-CELATE SUBUNIT CHD1 REVERSE	<i>Pseudomonas</i>	180	162 - 412	493 - 511	2	2.00E-21	•
•	►	CBB69268.1	Not given	<i>unidentified</i>	180	162 - 417	473 - 705	4	2.00E-40	•
•	►	AAE16669.1	CD16	<i>Escherichia coli</i>	170	254 - 417	15 - 172	2	6.00E-10	•
•	►	CAB58178.1	Mg-protoporphyrin IX	<i>Huicula</i>	170	162 - 410	90 - 311	4	2.00E-38	•
•	►	Q56284	thiopurine S-methyltransferase subunit	<i>Thiobacillus</i>	170	162 - 423	401 - 655	4	5.00E-38	•
•	►	BAA16787.1	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56285	thiopurine S-methyltransferase subunit	<i>Thiobacillus</i>	170	162 - 423	401 - 655	4	5.00E-38	•
•	►	Q56286	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56287	thiopurine S-methyltransferase subunit	<i>Thiobacillus</i>	170	162 - 423	401 - 655	4	5.00E-38	•
•	►	Q56288	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56289	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56290	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56291	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56292	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56293	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56294	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56295	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56296	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56297	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56298	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56299	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56300	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56301	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56302	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56303	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56304	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56305	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56306	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56307	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56308	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56309	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56310	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56311	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56312	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56313	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56314	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56315	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56316	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56317	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56318	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56319	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56320	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56321	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56322	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56323	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56324	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56325	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56326	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56327	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56328	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56329	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56330	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56331	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56332	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56333	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56334	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56335	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56336	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56337	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56338	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56339	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56340	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56341	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56342	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56343	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56344	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56345	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56346	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56347	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56348	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56349	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56350	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56351	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56352	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56353	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56354	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56355	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56356	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56357	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56358	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56359	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56360	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56361	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56362	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56363	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56364	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56365	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56366	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56367	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56368	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56369	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56370	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56371	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56372	Mg chelatase subunit	<i>Ssp.</i>	180	69 - 387	415 - 588	4	6.00E-38	•
•	►	Q56373	Mg chelatase subunit	<i>Ssp.</i>	180					

FIG. 15

AllEye output (December 13, 2000 3:07 PM)

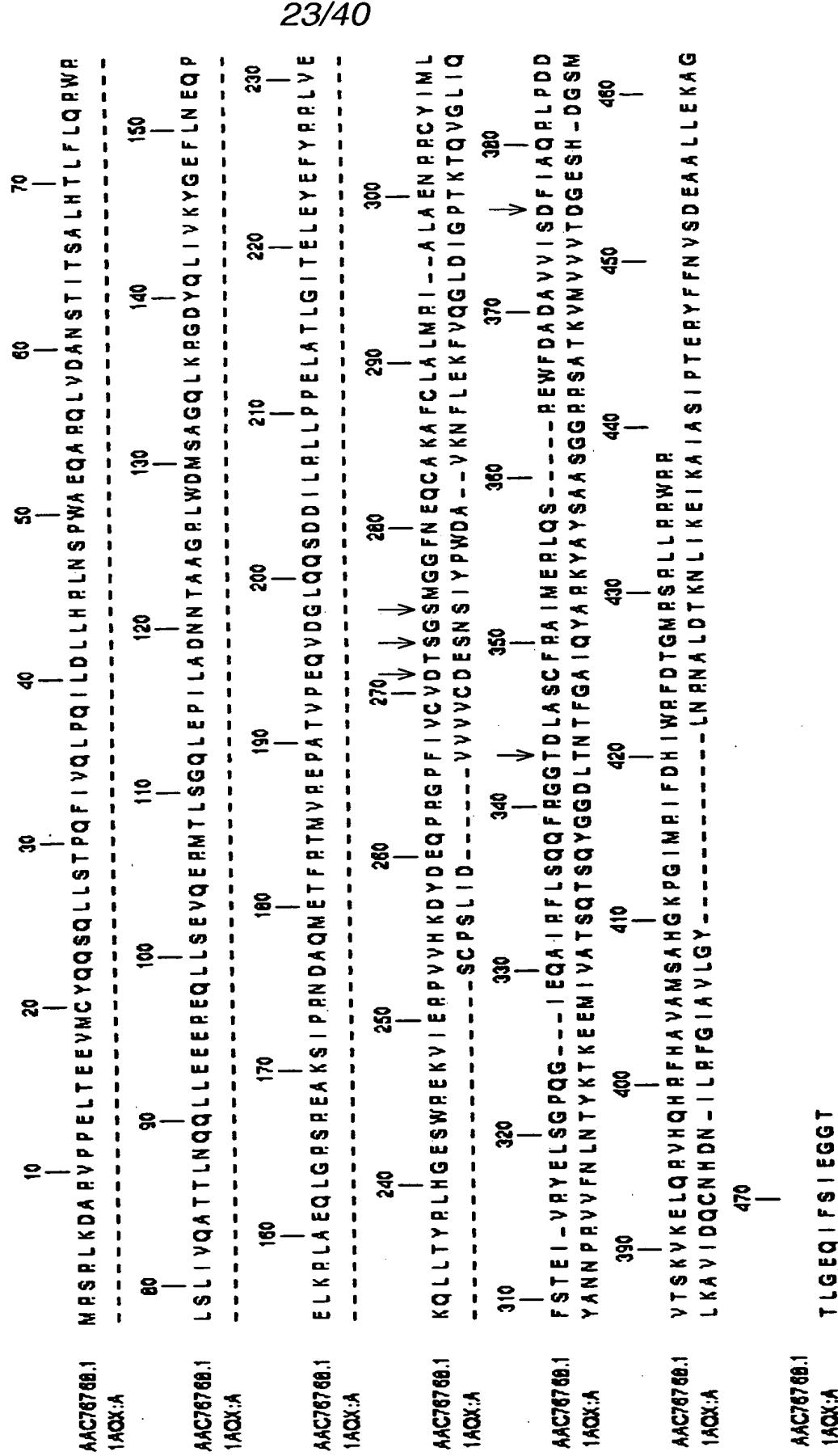
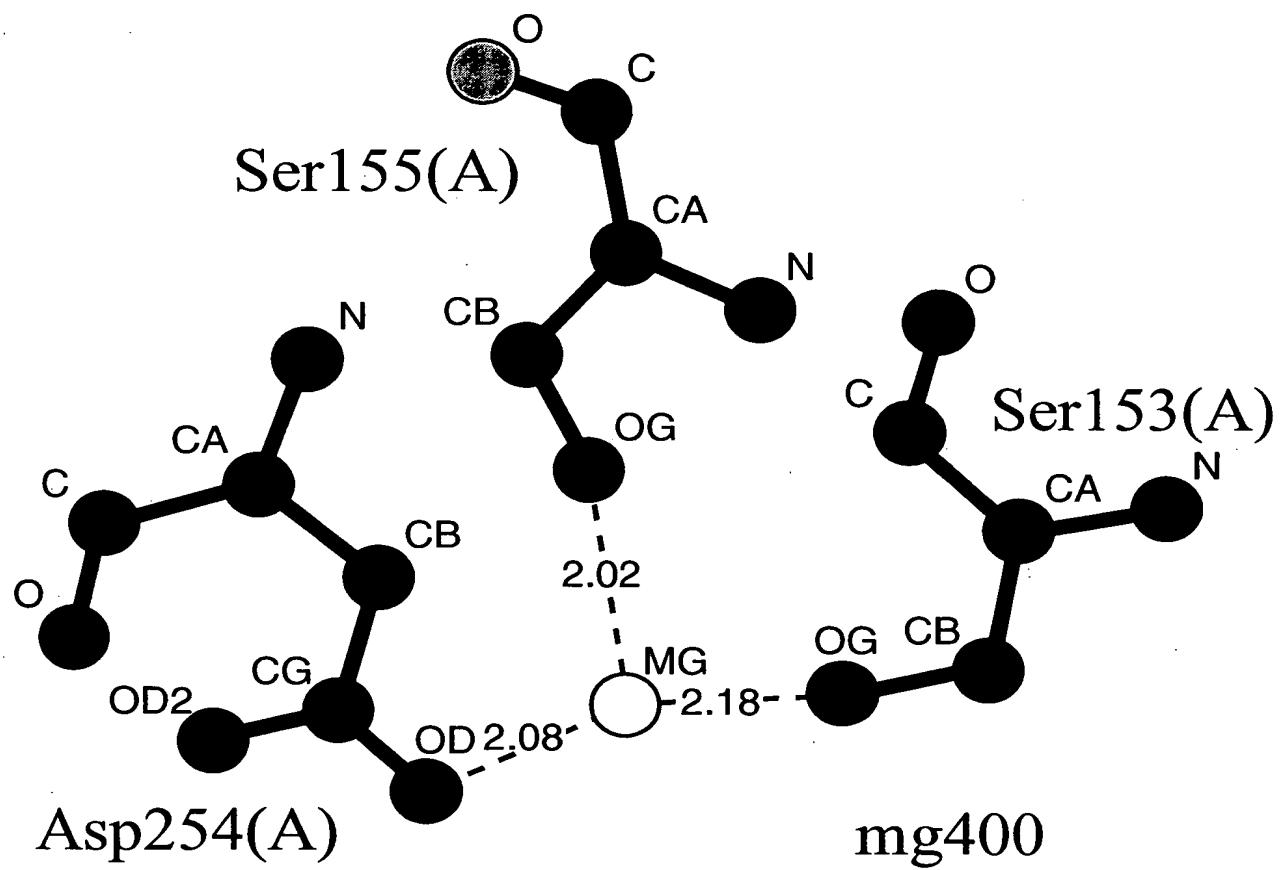


FIG. 16A



1aox: MG400

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FIG. 16B

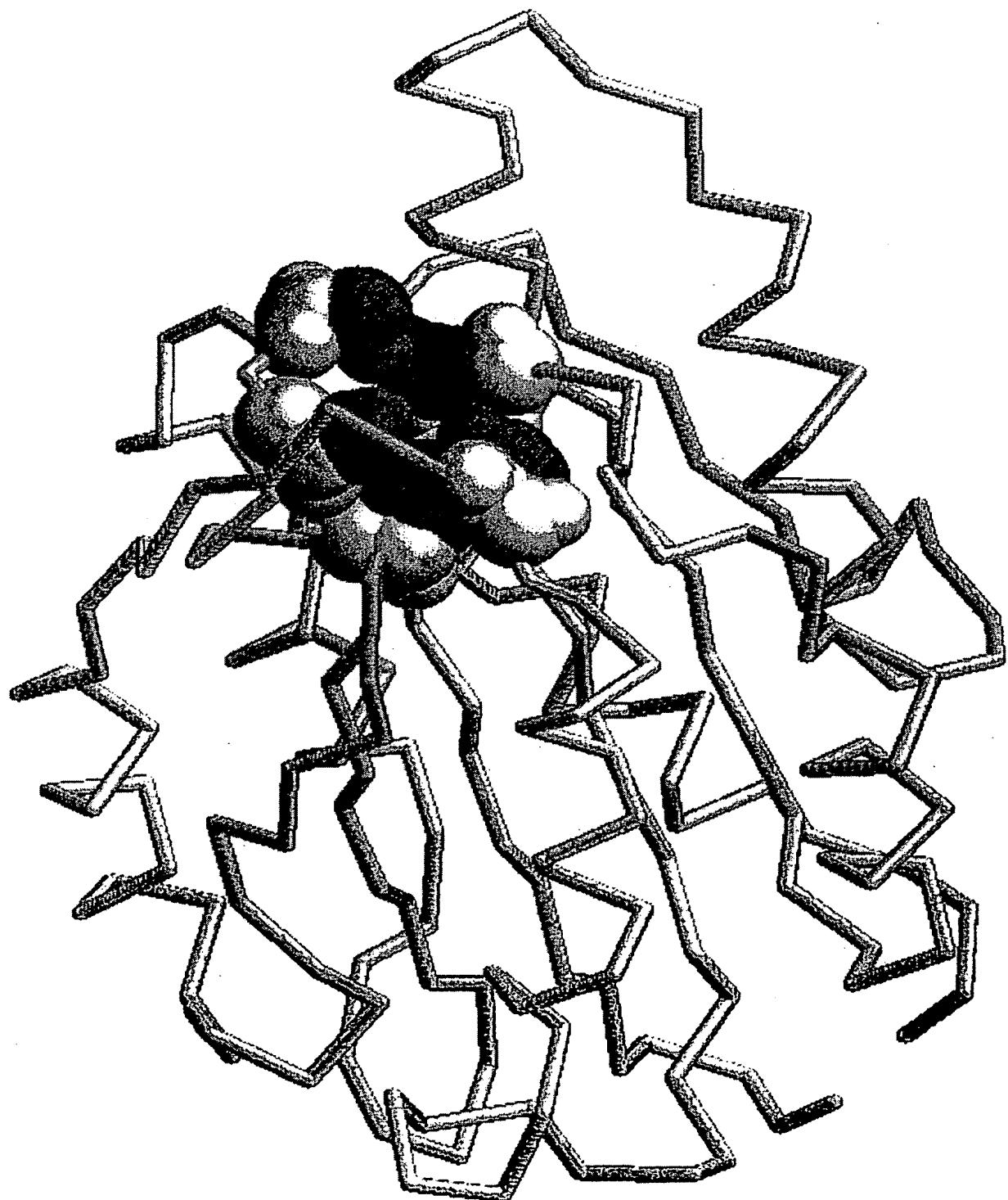
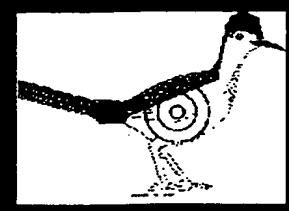


FIG. 17

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File Edit View Go Communicator Help

Bookmarks Location: <http://victoria.inpharmatica.co.uk/~volker/BPD3target.html>

 Target Mining Interface

 inpharmatica

Select Your Query Sequence

• Enter PDB accession number (e.g. 1QMA): and chain (e.g. B):

OR

• Enter one Swiss-Prot accession (e.g. P27504) or GenBank proteinID (e.g. CAB08761.1):

Select Database

Release:

Apply Filters

• Iteration Filter: PSI-BLAST matches to be excluded:

If you select e.g. "Matches detected during the first 3 iterations" these matches will be excluded from the report (using the first_PB_iter annotation). This allows you to focus on more remote homologous which have been detected after 4 or more PSI-BLAST iterations. Matches detected using PSI-BLAST with negative iterations or using Genome-Threader are not effected by this option. However, if one match is found during the first e.g. 3 PSI-BLAST iterations and by Genome-Threader it will be excluded.

• Filter for the following SPECIES:

Homo sapiens Rattus norvegicus (Rat) Mus musculus (Mouse) Danio rerio (Zebra fish)

100% 

FIG. 18A

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File Edit View Go Communicator Help

Back Forward Reload Home Search Netscape Print Security Stop

Bookmarks Location http://London-bridge.inpharmatica.co.uk/cgi-bin/volker/getTargetBPD3.pl

2) 81 additional hits identified by both, Genome Threader and PSI-BLAST:

Combined Genome Threader and PSI - Blast output: PSI - BLAST values are shown in maroon!

Add2list	BPD links	WWW link	Title	Organism	Div.	%ID (GT,PSI)	Query rgn. (GT,PSI)	Target rgn. (GT,PSI)	Ah. score (GT)	Conf. (GT)	1st iter. (PSI)
↓	AAA59544.1 drill through Top50Blast1Hits	AAA59544.1	Not given	Homo sapiens	PRI	100%, 100% unmaskedSW	1-187, 1-187	148-334, 148-334	488	100% unmaskedGT	1
→	AAB24821.1 drill through Top50Blast1Hits	AAB24821.1	leukocyte integrin alpha chain	Homo sapiens	PRI	100%, 100% unmaskedSW	1-187, 1-187	148-334, 148-334	488	100% unmaskedGT	1
↓	Q99715 drill through Top50Blast1Hits	Q99715	COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.	Homo sapiens (Human)	PRI	28.9%, 28% unmaskedSW	2-186, 2-179	439-617, 2322-2494	456	100% unmaskedGT	1
↓	AAB38702.1 drill through Top50Blast1Hits	AAB38702.1	cartilage matrix protein	Homo sapiens	PRI	28.9%, 25% unmaskedSW	2-186, 2-186	274-452, 40-221	446	100% unmaskedGT	1
↓	AAC01506.1 drill through Top50Blast1Hits	AAC01506.1	type XII collagen	Homo sapiens	PRI	28.4%, 28% unmaskedSW	2-186, 2-186	137-318, 137-318	445	100% unmaskedGT	1
↓	CAA72402.1 drill through Top50Blast1Hits	CAA72402.1	collagen type XIV	Homo sapiens	PRI	28.7%, 30% unmaskedSW	2-186, 2-186	6-185, 6-185	442	100% unmaskedGT	1
↓	AAB38547.1 drill through Top50Blast1Hits	AAB38547.1	leukointegrin alpha d chain	Homo sapiens	PRI	61%, 80% unmaskedSW	1-187, 1-187	148-334, 148-334	439	100% unmaskedGT	1
↓	CAB71222.1 drill through Top50Blast1Hits	CAB71222.1	dJ238D15.1 (collagen, type XII, alpha 1)	Homo sapiens	PRI	27.1%, 22% unmaskedSW	1-186, 2-186	293-472, 1430-1620	439	100% unmaskedGT	1
↓	CAA07569.1 drill through Top50Blast1Hits	CAA07569.1	matrin-4	Homo sapiens	PRI	27.9%, 24% unmaskedSW	2-186, 3-187	344-525, 34-215	418	100% unmaskedGT	2
↓	CAB46380.1 drill through Top50Blast1Hits	CAB46380.1	dJ453C12.3 (matrin-4)	Homo sapiens	PRI	27.9%, 24% unmaskedSW	2-186, 3-186	385-566, 34-214	418	100% unmaskedGT	2

FIG. 18B

				KIAA0336 protein		Homo sapiens	PRI	20.2%	Unmarked SW	73-165	390-503	66	Unmarked GI reverse HI
-	Red.Scr.View	drill through Tors50BlastH1a	BA031651.L			Homo sapiens	PRI	14.1%	Unmarked SW	6-88	20-105	76	68.6%
-	Red.Scr.View	drill through Tors50BlastH1a	CAE52192.L	G7c protein		Homo sapiens	PRI	14.1%	Unmarked SW	73-143	405-474	73	88.6%
-	Red.Scr.View	drill through Tors50BlastH1a	BA035699.L	N-copine		Homo sapiens	PRI	26.0%	Unmarked SW				Unmarked GI
-	Red.Scr.View	drill through Tors50BlastH1a	126012	INTEGRIN BETA-8 PRECURSOR.		Homo sapiens (Human)	PRI	13.1%	Unmarked SW	2-115	147-289	78	87.7%
-	Red.Scr.View	drill through Tors50BlastH1a	AA021820.L	NC37		Homo sapiens	PRI	14.1%	Unmarked SW	6-88	316-403	76	85.5%
-	Red.Scr.View	drill through Tors50BlastH1a	AA021820.L	Se23 protein		Homo sapiens	PRI	18.7%	Unmarked SW	7-141	134-275	74	84.4%
-	Red.Scr.View	drill through Tors50BlastH1a	CAE52751.L	copine 1		Homo sapiens	PRI	20%	Unmarked SW	73-165	384-487	87	80.7%
-	Red.Scr.View	drill through Tors50BlastH1a	AA035920.L	polymerase		Homo sapiens	PRI	18.1%	Unmarked SW	84-185	442-582	55	74.2%
-	Red.Scr.View	drill through Tors50BlastH1a	CA037610.L	4J09K20.3 (Copine (similar to KIAA0636))		Homo sapiens	PRI	25%	Unmarked SW	76-143	383-429	67	80.3%
-	Red.Scr.View	drill through Tors50BlastH1a	CA037610.L	Not given		Homo sapiens	PRI	11.1%	Unmarked SW	6-145	373-504	56	71.4%
-	Red.Scr.View	drill through Tors50BlastH1a	AA035532.L	60 kDa protein (60 kDa ribonucleoprotein (RNP) (Sjogren syndrome type A antigen (SS-A)))		Homo sapiens (Human)	PRI	11.1%	Unmarked SW	6-145	373-504	58	70.1%
-	Red.Scr.View	drill through Tors50BlastH1a	ED0155	Not given 1		Homo sapiens	PRI	18.5%	Unmarked SW	22-122	74-851	75	68.7%
-	Red.Scr.View	drill through Tors50BlastH1a	AA035833.L	KIAA1434 protein		Homo sapiens	PRI	20.8%	Unmarked SW	124-186	578-647	67	87.4%
-	Red.Scr.View	drill through Tors50BlastH1a	BA032672.L	Se24B protein		Homo sapiens	PRI	9%	Unmarked SW	6-91	682-801	61	61.4%
-	Red.Scr.View	drill through Tors50BlastH1a	CAA03351.L	proteolipin gamma A11		Homo sapiens	PRI	15.6%	Unmarked SW	30-85	475-843	66	88.6%
-	Red.Scr.View	drill through Tors50BlastH1a	AA037262.L	proteolipin gamma A11 short form protein		Homo sapiens	PRI	15.1%	Unmarked SW	30-85	475-843	66	88.6%
-	Red.Scr.View	drill through Tors50BlastH1a	AA043758.L	proteolipin gamma A11		Homo sapiens	PRI	10.2%	Unmarked SW	20-184	123-308	58	87.0%
-	Red.Scr.View	drill through Tors50BlastH1a	AA037214.L	annelin 3 (annelin XXXI)		Homo sapiens	PRI	18.5%	Unmarked SW	22-122	750-852	73	82.0%
-	Red.Scr.View	drill through Tors50BlastH1a	AA043714.L	hecidin 1		Homo sapiens	PRI	18.4%	Unmarked SW	2-55	152-204	67	88.6%
-	Red.Scr.View	drill through Tors50BlastH1a	AA0359185.L	Integrin beta-7 subunit		Homo sapiens	PRI	24.3%	Unmarked SW	2-36	130-168	73	88.9%
-	Red.Scr.View	drill through	AA0359211.L	Integrin related beta-5		Homo sapiens	PRI	20.2%	Unmarked SW				Unmarked GI

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FIG. 19

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Biopeidium additional annotation page - Netscape

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Bookmarks Location: ./london-bridge/inpharmatica/BPDDEV/cgibin/ssp/pl/7&ep.esn=55817&password=caiss_app&username=caiss_app&oracle_sid=BPDDEV

Aligned annotation view for P10155 (downloading image...)

Primary database information:

SWISSPROT

Secondary database information:

Positive matches

Prints matches

Inpharmatica calculated information

Inpharmatica results

Inpharmatica

Inpharmatica

Sequence information

Source database: SWISSPROT

Accession code: P10155

Gene name: SSA2/CEPRO60

Download sequence in FASTA format

Links to other resources:

View custom hyperlinks

Search in EXPASY

European Bioinformatics Institute

PRIDE

Online Mendelian Inheritance in Man

Online Mendelian Inheritance in Man

Protein Information Resource

Protein Information Resource

Swissprot comments:

FUNCTION UNKNOWN

43 SMALL RIBONUCLEOPROTEINS CONSIST OF FOUR SMALL RNA MOLECULES OF 85-112 NT EACH OF

Document Done

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FIG. 20

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Bookmarks Location: http://www.sanger.ac.uk/cgi-bin/Pfam/nph-search.cgi

The Sanger Centre **Pfam**
Protein families database of alignments and HMMs

Home | Keyword search | Protein search | DNA search | Browse Pfam | Taxonomy search | Help

Results for gi|133251|sp|P10155|RO60_HUMAN

There were no matches to Pfam-A (including borderline matches) for gi|133251|sp|P10155|RO60_HUMAN

Matches to Pfam-B

Domain	Start	End	Evalue	Alignment
Pfam-B_8344	1	194	2.3e-103	Align
Pfam-B_10162	195	538	1.8e-165	Align

[538 residues]

Alignments of Pfam-B domains to best-matching Pfam-B sequence

Format for fetching alignments to Pfam-B families: Hypertext linked to swisspfam

Query gi|133251|sp|P10155|RO60_HUMAN/1-194 matching Pfam-B_8344

Q92787	1	MEESVNQM QPLNEKQIANSQDG YVWQVTDNRLMRFLCF GSEGGTYYIKE	50
gi 133251 sp P10155 RO60_HUMAN	1	MEESVNQM QPLNEKQIANSQDG YVWQVTDNRLMRFLCF GSEGGTYYIKE	50
Q92787	51	QKL GLENREALIRLIEDGRG CEVIVQEI KSF S QEGRTTK QEPMLF ALA ICS	100
gi 133251 sp P10155 RO60_HUMAN	51	QKL GLENREALIRLIEDGRG CEVIVQEI KSF S QEGRTTK QEPMLF ALA ICS	100
Q92787	101	QCSDISTK QAAFKAV SEV CRIPTM LPTFI QPKKD LKE SMKC G W G R A L R K	150
gi 133251 sp P10155 RO60_HUMAN	101	QCSDISTK QAAFKAV SEV CRIPTM LPTFI QPKKD LKE SMKC G W G R A L R K	150
Q92787	151	R I A D W Y R E K G G M A L A L A R T K Y K Q R N G W S M K D L L R L S M L K P S S E G	194
gi 133251 sp P10155 RO60_HUMAN	151	R I A D W Y R E K G G M A L A L A R T K Y K Q R N G W S M K D L L R L S M L K P S S E G	194

Query gi|133251|sp|P10155|RO60_HUMAN/195-538 matching Pfam-B_10162

008848	195	L A I V T K Y I T K G W K E V I M E E Y K E K A L S V E A K L L K Y L E A V E K V K R T K D D L E V	244
gi 133251 sp P10155 RO60_HUMAN	195	L A I V T K Y I T K G W K E V I M E E Y K E K A L S V E A K L L K Y L E A V E K V K R T K D D L E V	244
008848	245	I M L I E E M Q L V R E M L L T H M L K S K E V V K A L L Q E M P L T A L L R N L G K M T A N S V L	294
gi 133251 sp P10155 RO60_HUMAN	245	I M L I E E M Q L V R E M L L T H M L K S K E V V K A L L Q E M P L T A L L R N L G K M T A N S V L	294
008848	295	E P G N S E V S L I C E K L S N E K L L K K A R I M P F H V L I A L E T Y R A G M G L R G K L K W I	344
gi 133251 sp P10155 RO60_HUMAN	295	E P G N S E V S L I C E K L S N E K L L K K A R I M P F H V L I A L E T Y R A G M G L R G K L K W I	344
008848	345	P D K D I L Q A L D A R P Y T I F K I V E P T G K R F L L A V D V S A S M N Q R A L G S V L R A S T	394

FIG. 21

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Bookmarks Location http://www.ncbi.nlm.nih.gov:80/entrez/query.fcgi?cmd=Retrieve&db=Prot

LOCUS R060_HUMAN 538 aa **PRI** 01-FEB-1996
DEFINITION 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (R0RNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)).

ACCESSION P10155
PID g133251
VERSION P10155 GI:133251
DBSOURCE swissprot: locus R060_HUMAN, accession P10155:
 class: standard.
 created: Mar 1, 1989.
 sequence updated: Mar 1, 1989.
 annotation updated: Feb 1, 1996.
 xrefs: gi: gi: 177782, gi: gi: 177783, gi: gi: 387656, gi: gi: 387657, gi: gi: 86722, gi: gi: 107626
 xrefs (non-sequence databases): MIM 600063, MIM 234700, PROSITE P500030

KEYWORDS Ribonucleoprotein; RNA-binding; Systemic lupus erythematosus; Antigen.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 538)
AUTHORS Deutscher, S.L., Harley, J.B. and Keene, J.D.
TITLE Molecular analysis of the 60-kDa human Ro ribonucleoprotein
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 85 (24), 9479-9483 (1988)
MEDLINE 89071722
REMARK SEQUENCE FROM N.R.
REFERENCE 2 (residues 1 to 538)
AUTHORS Ben-Chetrit, E., Gandy, B.J., Tan, E.M. and Sullivan, K.F.
TITLE Isolation and characterization of a cDNA clone encoding the 60-kD component of the human SS-R/Ro ribonucleoprotein autoantigen
JOURNAL J. Clin. Invest. 83 (4), 1284-1292 (1989)
MEDLINE 89198084
REMARK SEQUENCE FROM N.R.
COMMENT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] UNKNOWN.
 [SUBUNIT] RO SMALL RIBONUCLEOPROTEINS CONSIST OF FOUR SMALL RNA MOLECULES OF 85-112 NT, EACH OF WHICH IS COMPLEXED WITH A 60 KD PROTEIN. RO RNPs MAY ALSO CONTAIN AN ADDITIONAL 52 KD PROTEIN.
 [SUBCELLULAR LOCATION] CYTOPLASMIC.
 [DISEASE] SERA FROM PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS OFTEN CONTAIN ANTIBODIES THAT REACT WITH THE NORMAL CELLULAR RO PROTEIN AS IF THESE ANTIGEN WAS FOREIGN.
 [SIMILARITY] CONTAINS 1 RNA RECOGNITION MOTIF (RNP).
 [SIMILARITY] STRONG, TO XENOPUS 60 KD RO PROTEIN.

FEATURES Location/qualifiers
source 1..538
 /organism="Homo sapiens"
 /db_xref="taxon: 9606"
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Protein 1..538
 /product="60 KD RO PROTEIN"
Region 93..98
 /region_name="Domain"
 /note="RNA-BINDING (RNP2) (BY SIMILARITY)."
Region 124..131
 /region_name="Domain"
 /note="RNA-BINDING (RNP1) (BY SIMILARITY)."
Region 239
 /region_name="Conflict"
 /note="K -> R (IN REF. 2)."
Region 515..538
 /region_name="Conflict"
 /note="GMLDMCCGFDTCALDVIRNPTLDMI -> RLQNTLNLKSP (IN REF. 2)."
ORIGIN
 1 meesvngmqp lnekqiansq dgyvwqvtmdn nrlhrflcfg seggtyyike qklgleneaa
 61 lirliedgrg ceviqeqiksf sqegrttkqe pmlfalaics qcsdistkqa afkavsevcr
 121 ipthlftfq fkkdikesmk cgmwgralrk aiadwpynekg gmalalavtk ykqrngwshk
 181 dlrlrlshlkp ssegglaiytk yitkgwkevh elykekalsv etekllkyle avekvkrtd
 241 elevihliee hrlvrehllit nhlkskeuwk allqemplta llrnlgkmta nsylepgnse
 301 vslvceklnn ekllkkarih pfhilialet yktghglrgk lkwrpdeeil kaldaafykt
 361 fktveptgkr fllavdvsa mnqrvlgsil nastvaaamc msvtrtekds yvvafsdemv
 421 pcpvttdntl qgvimamsqi paggtcdslp miwakqkntp advfivftdn etfaggvhpa
 481 iaireyrkkn dipaklivcg mtsngftiad pddrgmildmc gfdtgaldvi rntfildmi
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FIG. 22A

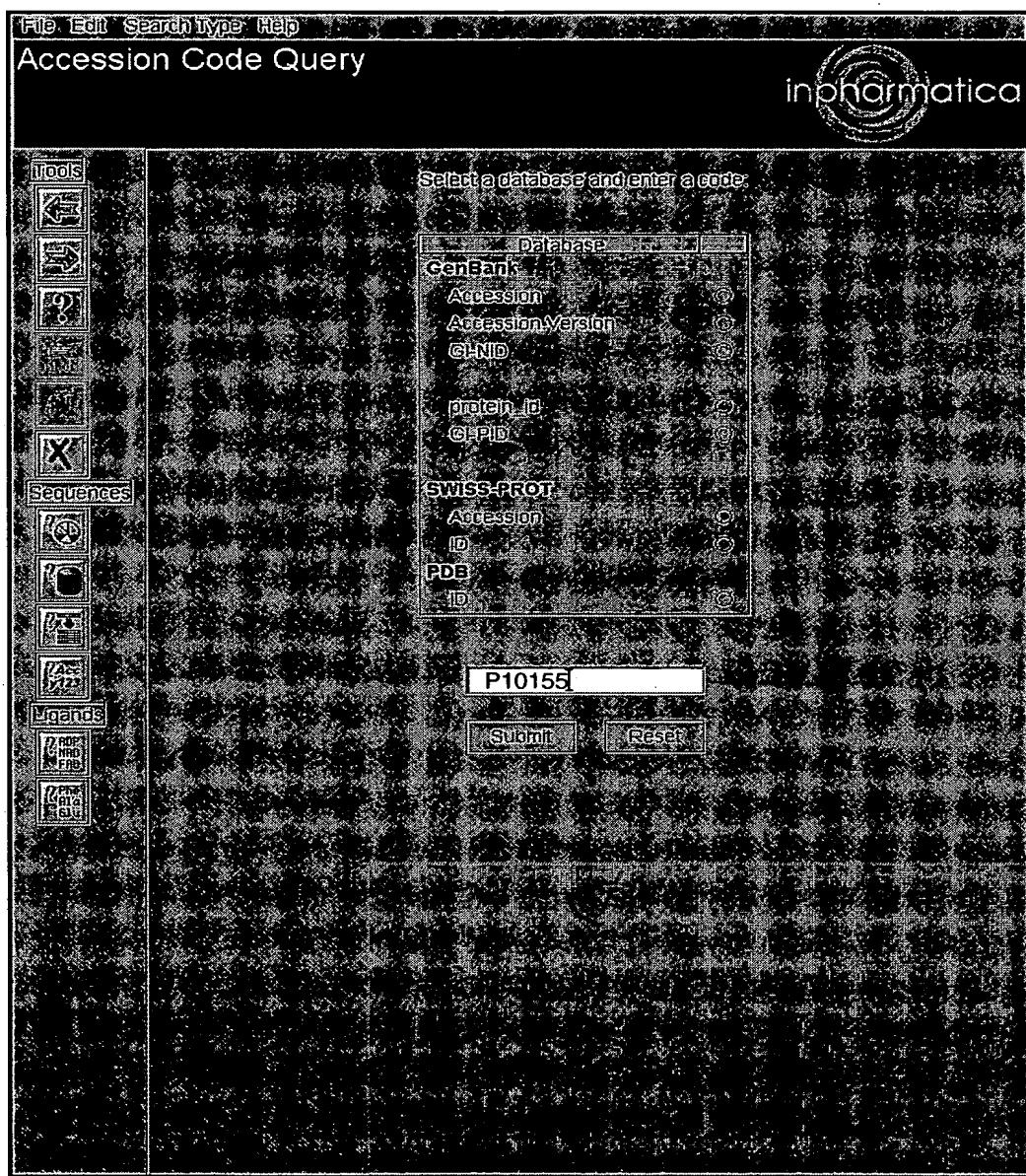


FIG. 22B Aligned Sequence Display

Query details:

P10155: 60 KDa/RO PROTEIN (60 KDa RIBONUCLEOPROTEIN RO) (RORNP) (SJORGREN SYNDROME TYPE A ANTIGEN (SS-A)).

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Page 1 of 2 Total hits: 31 Selected: 1

Total Selected 31 Selected 1 Detailed

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inpharmatica Genome Threader results

Cluster/Detail	Contig	Start	End	Strand	Organism	2D Query	2D Threader	Min. score	Method	Confidence
•	1BHQ1	16	104	+	<i>S. enterica</i>	16 - 104	16 - 104	54	Local	Low (75%)
•	1BHQ1	16	104	+	<i>S. enterica</i>	16 - 104	16 - 104	55	Local	Low (70%)
•	1BHQ1 MAC-1 DOMAIN MAGNESIUM COMPLEX	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1BHQ2 MAC-1 DOMAIN MAGNESIUM COMPLEX	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1DN2 MAC-1 DOMAIN METAL FREE	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1BHQ2 MAC-1 DOMAIN CADMIUM COMPLEX	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1BHQ1 MAC-1 DOMAIN CADMIUM COMPLEX	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1DN1 MAC-1 DOMAIN METAL FREE	117	313	-	<i>H. sapiens</i>	117 - 313	504 - 515	55	Local	Low (67%)
•	1BHLA TRP SYNTHASE (DSN-IPP-SER) WITH K+	105	24	-	<i>S. pombe</i>	105 - 24	102 - 248	53	Local	Low (55%)
•	1DOD2 I-E-DOMAIN FROM INTEGRIN GENE BONE	103	313	-	<i>H. sapiens</i>	103 - 313	389 - 391	51	Local	Low (55%)
•	2TSA X-RAY CRYSTAL STRUCTURE OF MUTANT (BETA A) TRYPTOPHAN SYNTHASE (EC.4.2.120) WITH I-E-DOMAIN FROM INTEGRIN GENE BONE	115	25	-	<i>H. sapiens</i>	115 - 25	174 - 103	55	Local	Low (55%)
•	2TSA X-RAY CRYSTAL STRUCTURE OF MUTANT (BETA A) TRYPTOPHAN SYNTHASE (EC.4.2.120) WITH I-E-DOMAIN FROM INTEGRIN GENE BONE	115	25	-	<i>H. sapiens</i>	115 - 25	174 - 103	55	Local	Low (55%)
•	1UBSA TRYPTOPHAN SYNTHASE (EC.4.2.120) WIT	115	42	-	<i>S. pombe</i>	115 - 42	174 - 120	55	Local	Low (45%)
•	1BSC1 TRYPTOPHAN SYNTHASE (EC.4.2.120) FROM S. POMBE	105	22	-	<i>S. pombe</i>	105 - 22	17 - 251	55	Local	Low (35%)
•	1OAKA CRYSTAL STRUCTURE OF THE VON WILLEBRAND FACTOR	6.7	386	-	<i>H. sapiens</i>	6.7 - 386	504 - 515	49	Local	Low (34%)
•	1AOBK CRYSTAL STRUCTURE OF THE VON WILLEBRAND FACTOR	103	41	-	<i>H. sapiens</i>	103 - 41	504 - 515	49	Local	Low (34%)
•	1QGP1 STRUCTURE OF THE COMPLEX OF AN FAB	21.1	277	-	<i>F. saccharinum</i>	21.1 - 277	355 - 100	82	Local	Low (25%)
•	1EYD1 TRYPTOPHAN SYNTHASE (EC.4.2.120) FROM F. SACCHARINUM	21.1	277	-	<i>F. saccharinum</i>	21.1 - 277	355 - 100	82	Local	Low (25%)
•	1AUG1 CRYSTAL STRUCTURE OF VON WILLEBRAND FACTOR	7.0	313	-	<i>H. sapiens</i>	7.0 - 313	504 - 515	49	Local	Low (21%)
•	1BWE1 CRYSTAL STRUCTURE OF VON WILLEBRAND FACTOR	7.0	313	-	<i>H. sapiens</i>	7.0 - 313	504 - 515	49	Local	Low (21%)
•	1ITPA TRYPTOPHAN SYNTHASE (EC.4.2.120) IN T. SODIUM	10.4	44	-	<i>T. sodium</i>	10.4 - 44	172 - 122	51	Local	Low (15%)
•	1ITPA TRYPTOPHAN SYNTHASE (EC.4.2.120) IN T. SODIUM	10.4	44	-	<i>T. sodium</i>	10.4 - 44	172 - 251	51	Local	Low (15%)
•	1ART1 ASPARTATE AMINO TRANSFERASE (EC.2.6.1.52)	10.5	405	-	<i>E. coli</i>	10.5 - 405	537 - 548	52	Local	Low (15%)
•	1QTE1 ASPARTATE AMINO TRANSFERASE FROM E. COLI	10.5	405	-	<i>E. coli</i>	10.5 - 405	537 - 548	52	Local	Low (15%)
•	1EEA1 CRYSTAL STRUCTURE OF YEAST KARYOP	155	35	-	<i>S. cerevisiae</i>	155 - 35	150 - 238	49	Local	Low (10%)
•	1EEB1 CRYSTAL STRUCTURE OF YEAST KARYOP	155	35	-	<i>S. cerevisiae</i>	155 - 35	150 - 238	49	Local	Low (10%)
•	1AHP1 ASPARTATE AMINO TRANSFERASE Y225R	105	405	-	<i>E. coli</i>	105 - 405	537 - 548	52	Local	Low (10%)
•	1AHP1 ASPARTATE AMINO TRANSFERASE Y225R	105	405	-	<i>E. coli</i>	105 - 405	537 - 548	52	Local	Low (10%)
•	1EF1A1 CRYSTAL STRUCTURE OF THE MOSSIN F...	18.8	82	-	<i>A. thaliana</i>	18.8 - 82	171 - 188	55	Local	Low (10%)
•	1EF1S1 CRYSTAL STRUCTURE OF THE MOSSIN F...	18.8	82	-	<i>A. thaliana</i>	18.8 - 82	171 - 188	55	Local	Low (10%)

Tools

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GenBank ▶ SWISS-PROT ▶ PDB

FIG. 220 Aligned Sequence Display

Query details: P10155:60

PROTEIN 60 KDA E0 PROTEIN (60 KDA RIBONUCLEOPROTEIN) (SORGEN SYNDROME TYPE A ANTIGEN (SS-A))

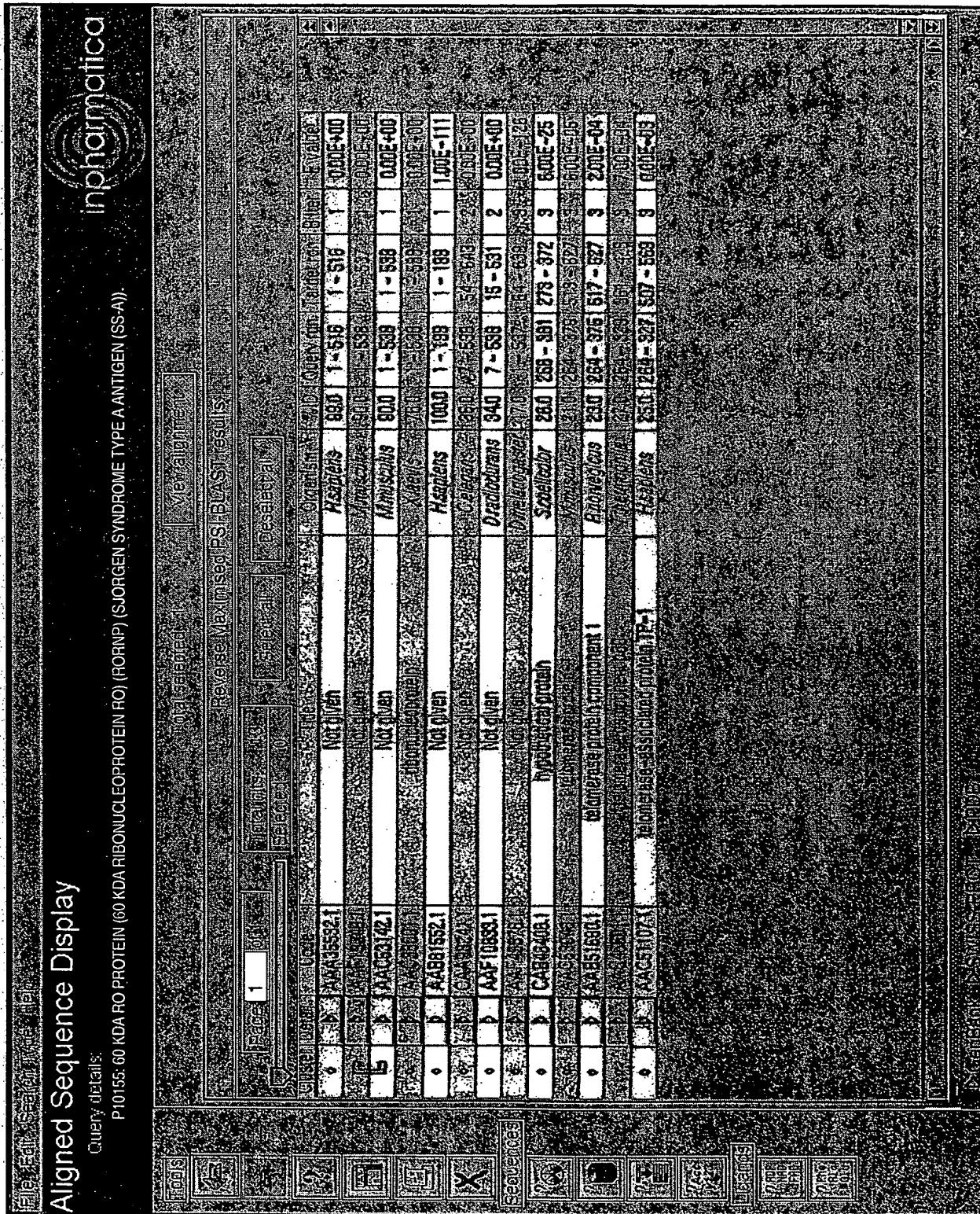


FIG. 23

AIEye output (January 2, 2001 1:29 PM)

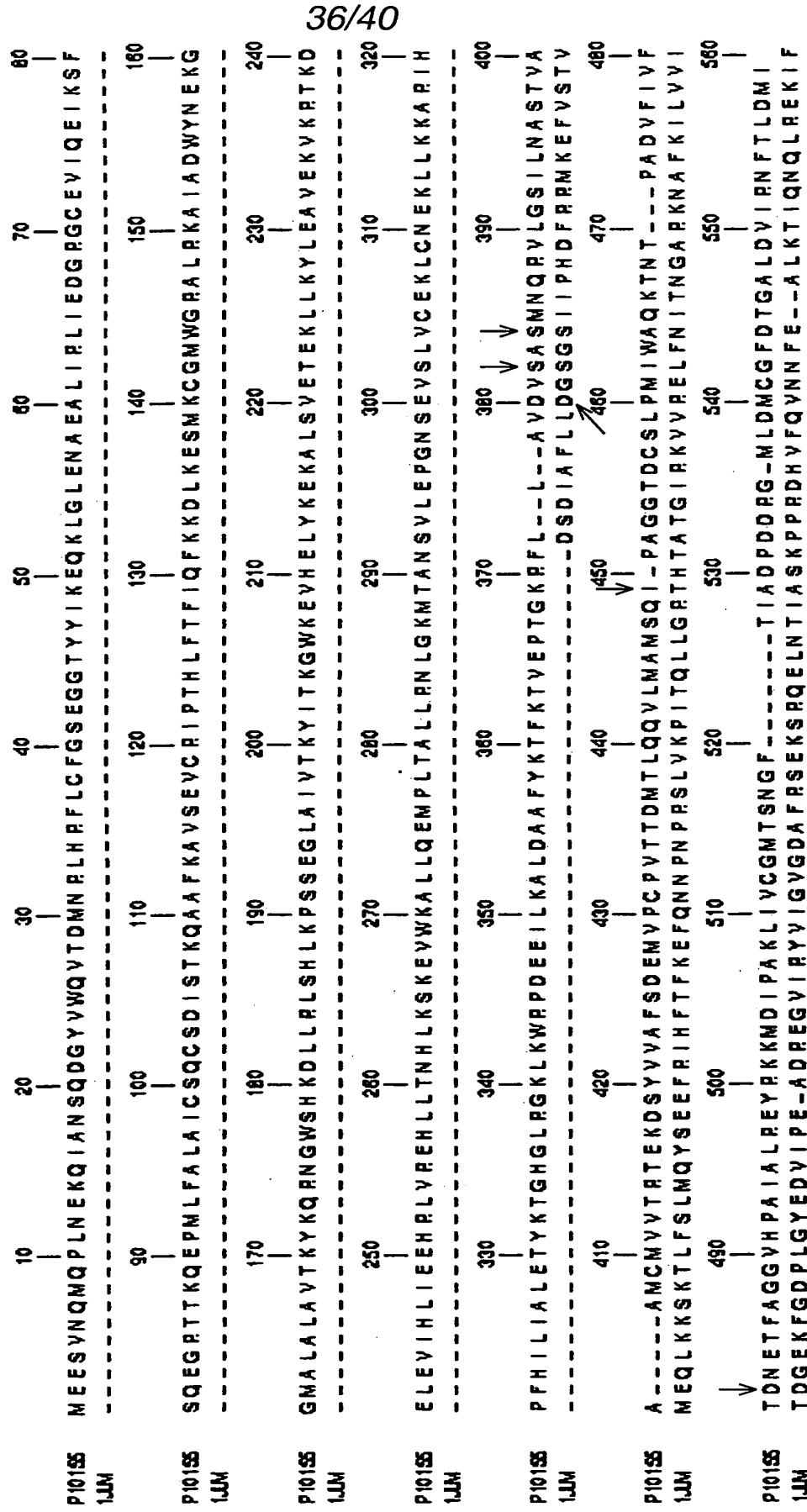
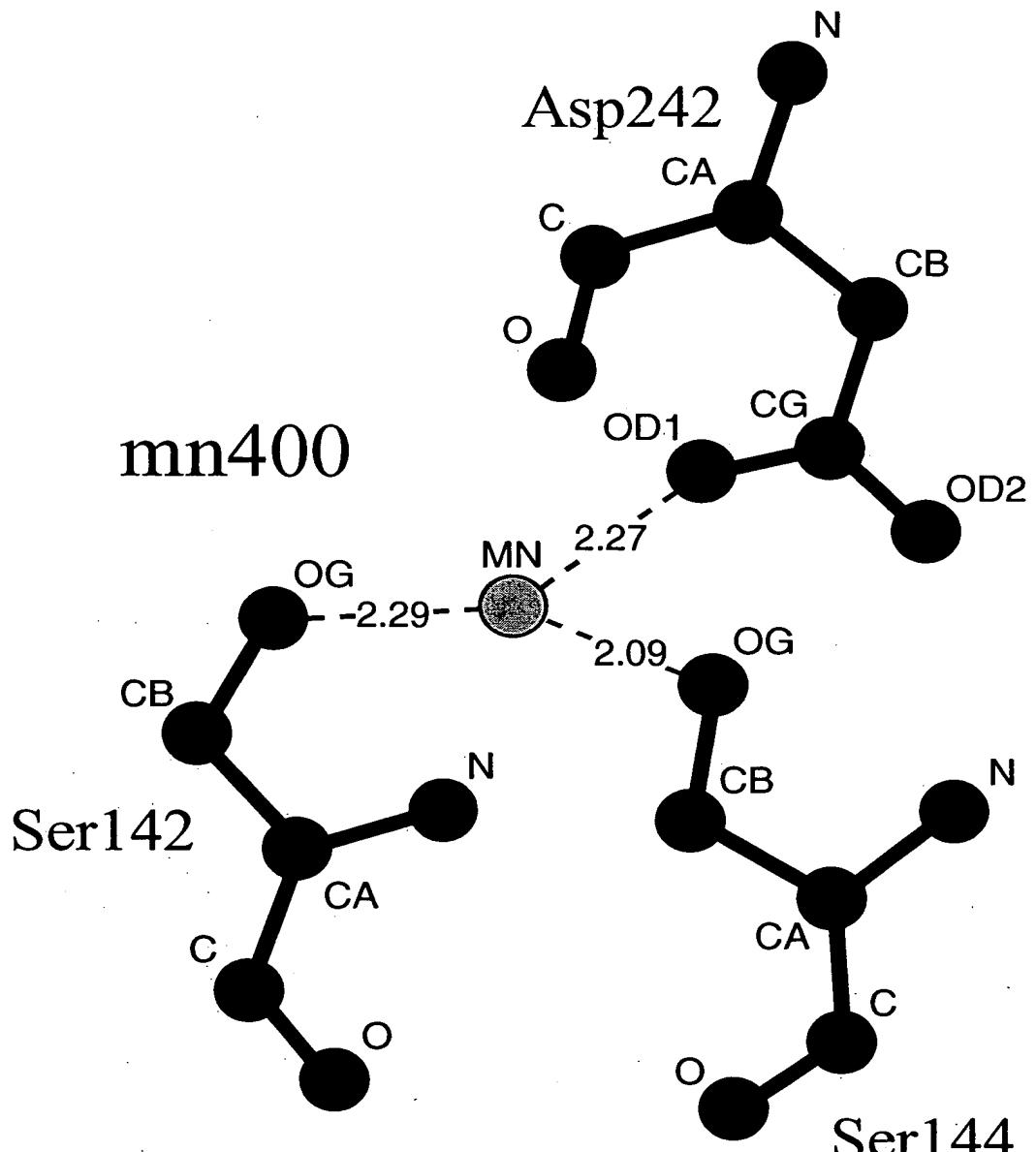


FIG. 24A



1jlm: MN 400

FIG. 24B

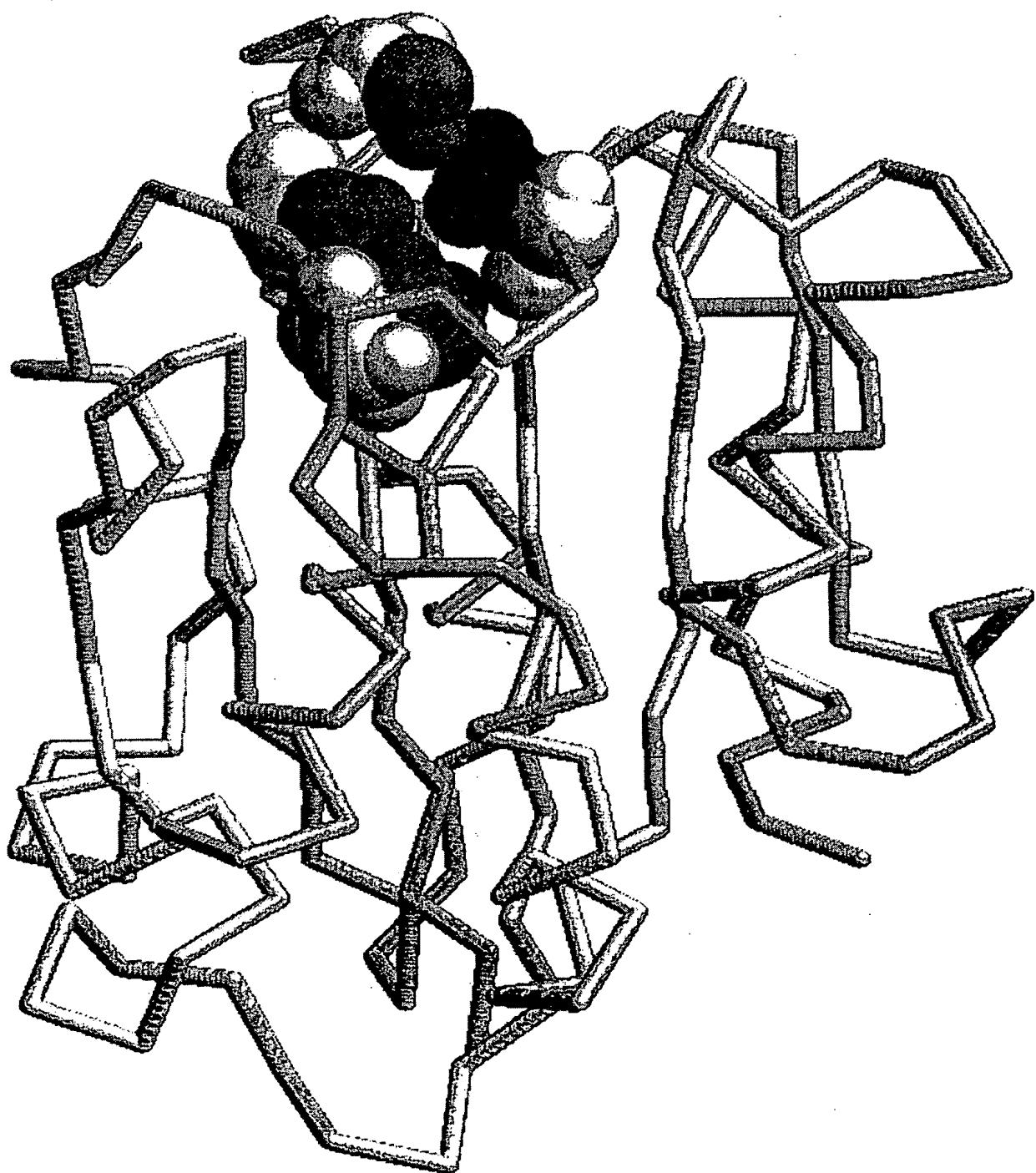


FIG. 25

AIEye output (January 4, 2001 3:18 PM)

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FIG. 25 (contd.)

AIEye output (January 4, 2001 3:18 PM)

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P10155 A M S Q I P A G G T D C S L P M I W A Q K T N T P A D V F I V F T D N E T F A G G V H P A I A L R E Y R K K M D I - P A K L I V C G M T S N G F T I A D P D
AAF19049.1 A M N K V P A G N T D C S L P M I W A Q K T G T A D V F I V F T D N E T F A G Q V H P A V A L R E Y R K K M D I - P A K L I V C G M T S N G F T I A D P D
AAC38001.1 K M S D I T M G S T D C A L P M L W A Q K T N T A D I F I V F T D C E T N V E D V H P A T A L K Q Y R E K M G I - P A K L I V C A M T S N G F S I A D P D
CAA98241.1 Y V N N L D F G R T D C G L P M T W A T E N N L K F D V F I I Y T D N D T W A G E I H P F E A I K K Y R E A S G I H D A K V I V M A M Q A Y D Y S I A D P S
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AAC38001.1 D R G M L D I C G F D S G A L D V I R N F T L D L I
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